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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
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KNOBBE, MARTENS, OLSON & BEAR, LLP
2040 MAIN STREET
IRVINE, CA 92614

EXAMINER	
DUFFY, PATRICIA ANN	

ART UNIT	PAPER NUMBER
1645	

DATE MAILED: 08/29/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/063,692	EATON ET AL.	
	Examiner	Art Unit	
	Patricia A. Duffy	1645	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☐ Responsive to communication(s) filed on _____.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-20* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-20* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☒ The drawing(s) filed on *08 May 2002* is/are: a)☒ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449 or PTO/SB/08) Paper No(s)/Mail Date *2002*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____.
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☒ Other: *sequence attachments*.

DETAILED ACTION

The preliminary amendments filed 9-10-02 has been entered into the record. Claims 1-20 are pending.

Priority

Applicant's claim for domestic priority under 35 U.S.C. 119(e) is acknowledged. However, the provisional application upon which priority is claimed fails to provide adequate support under 35 U.S.C. 112 for claims 1-20 of this application.

According to the priority statement of 9/10/02, it appears that the claimed subject matter defined in the instant application is not supported by the parent application serial no. 10/006,867. Based on the information given by applicant and an inspection of the patent applications, the examiner has concluded that the subject matter defined in this application is not supported by the disclosure in any of the applications for which Applicants claim priority because the claimed subject matter does not have utility, enablement or written description in any of the prior applications for reasons set forth herein. Accordingly, the subject matter defined in claims 1-20 has an effective filing date of 5-8-02.

Should the applicant disagree with the examiner's factual determination above, it is incumbent upon the applicant to provide the serial number and specific page number(s) of any parent application filed prior to 5-8-02 which specifically supports the particular claim limitation for each and every claim limitation in all the pending claims which applicant considers to have been in possession of and fully enabled for prior to 5-8-02.

Drawings

The drawings in this application have been approved by the Draftsperson. No further action is required by Applicants.

Specification

The disclosure is objected to because of the following informalities:

The lengthy specification has not been checked to the extent necessary to determine the presence of all possible minor errors. Applicant's cooperation is requested in correcting any errors of which applicant may become aware in the specification.

The title and abstract of the invention are not descriptive of the now claimed invention. A new title and abstract are required that is clearly indicative of the invention to which the claims are directed.

The disclosure is objected to because it contains an embedded hyperlink and/or other form of browser-executable code at least at page 35. Applicant is required to delete the embedded hyperlink and/or other form of browser-executable code. See MPEP § 608.01. Applicants should review the lengthy specification for other browser-executable code and delete or amend appropriately.

The use of the trademark ATCC™ has been noted in this application. They should be capitalized wherever it appears and be accompanied by the generic terminology.

Although the use of trademarks is permissible in patent applications, the proprietary nature of the marks should be respected and every effort made to prevent their use in any manner which might adversely affect their validity as trademarks. For example, the trademark American Type Culture Collection (ATCC ™) needs to be recognized wherever it appears.

Information Disclosure Statement

The information disclosure statement filed 9-17-02 has been considered with the exception of the BLAST sequences. The BLAST results demonstrate that applicants are ware of nucleic acids with identity/homology to the one claimed herein. However, as the BLAST results do not give sufficient identifying information, the Examiner cannot determine if said sequences constitute prior art.

An initialed copy is enclosed.

Claim Objections

Claims 1-20 are objected to because of the following informalities: the claims improperly reference Figures. Referencing figures in a claim is only proper when the information contained therein cannot be represented in any other manner (MPEP 2173.05(s)). Further, the sequence rules require sequences to be claimed by their appropriate sequence identifier number and not Figure number. Appropriate correction is required.

Claim Rejections - 35 USC § 101

35 U.S.C. 101 reads as follows:

Whoever invents or discovers any new and useful process, machine, manufacture, or composition of matter, or any new and useful improvement thereof, may obtain a patent therefore, subject to the conditions and requirements of this title.

The pending claims have been reviewed in light of the Utility Examination Guidelines and Guidelines for Examination of Patent Applications under 35 USC 112, first paragraph, "Written Description" Requirement, Federal Register, Vol. 66, No. 4, pages 1092-111, Friday, January 5, 2001.

Claims 1-20 are rejected under 35 U.S.C. 101 because the claimed invention lacks patentable utility due to its not being supported by a specific, substantial and credible utility or, in the alternative a well-established utility.

The claims are drawn to a nucleic acid encoding the polypeptide shown in Figure 38 (SEQ ID NO:38), fragments and percentage variants thereof encoded by SEQ ID NO:38. The nucleic acid of SEQ ID NO:37 corresponds to PRO1344 a cDNA corresponding to DNA 58723-1588 referenced in the specification. The specification does not disclose any secondary or tertiary structural features of this polypeptide, nor does it assert that the polypeptide has any homology with known, characterized polypeptides. The instant specification does not disclose any additional information regarding PRO1344 such as subcellular location, timing of regulation during cellular differentiation, which hormones or transcription factors regulate PRO1344, and what physiological significance PRO1344 plays. Therefore, it is a totally new, uncharacterized polynucleotide and polypeptide with no well-established utility.

The specification generally asserts that all of the disclosed PRO polynucleotides will be useful for a number of purposes; however, none of these asserted uses meet the three-pronged requirement of 35 U.S.C. § 101 regarding utility, namely, that the asserted utility be credible, specific and substantial. The asserted utilities will each be addressed in turn.

1) the PRO polynucleotide can be used as hybridization probes to isolate similar sequences, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, and in the recombinant production of the encoded polypeptide: This asserted utility is not specific or substantial. Since the same can be done with any polynucleotide, the asserted utility is not specific to the claimed PRO1344 polynucleotides. Furthermore, since the specification does not disclose how PRO1344 can be used, significant further research would be required of the skilled artisan to determine how to use the

polynucleotide or the encoded polypeptide. Since the asserted utility is not presented in a ready to use, real-world application, the asserted utility is not substantial.

2) the PRO polynucleotide can be used to make knock-in or knock-out transgenic animals: This asserted utility is not specific or substantial. Since the same can be done with any polynucleotide, the asserted utility is not specific. Also, the specification does not provide any information regarding the phenotype of the resulting animals, or what they can be used for (e.g., a model system for a specific disease). Therefore, the asserted utility is not substantial, as further research would need to be done before the asserted utility is in currently available form.

3) the PRO polynucleotide can be used in gene therapy: This asserted utility is not specific or substantial. Since a defect in any polypeptide is likely to cause a disease of some sort, every polynucleotide encoding a polypeptide is a target for gene therapy. Thus, the asserted utility is not specific to the claimed PRO1344 polynucleotide. Furthermore, the specification does not disclose a nexus between any specific disease states and a change in amount or form of PRO1344. Significant further research would have to be conducted to identify such a nexus. Therefore, the asserted utility is not substantial.

4) the PRO polynucleotide can be used in tissue typing: This asserted utility is not specific or substantial. With the exception of a few housekeeping genes, all polynucleotides have a tissue specific pattern of expression, and thus virtually any polynucleotide can be used in tissue typing. Thus, the asserted utility is not specific to PRO1344.

5) the PRO polynucleotide can be used to screen for compounds that interact with it: Since the same can be done with any polynucleotide, the asserted utility is not specific to the claimed PRO1344 polynucleotides. Furthermore, since no activity has been assigned to PRO1344, the compounds identified by such screening would have to be subjected to rigorous experimentation to determine how they are useful. Therefore, the asserted utility is also not substantial.

6) the Pro polynucleotide can be used in tumor/cancer diagnostics or therapeutics: The specification also discloses that PRO1344 was tested using quantitative PCR amplification reactions with cDNA libraries isolated from different human tumor and normal human tissue samples and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the nucleic acid encoding the PRO polypeptide (specification page 140). The specification teaches that the differential expression in one or more tumor tissues as compared to one or more normal tissues of the same tissue type renders the molecule useful diagnostically for the determination of the presence or absence of tumor in a subject suspected of possessing a tumor as well as therapeutically as a target for the treatment of a tumor in a subject possession such a tumor. mRNA encoding the PRO1344 polypeptide (DNA58723-1588) was reported as "more highly expressed in" normal stomach, kidney tumor and normal skin as compared to a stomach tumor, normal kidney and melanoma tumor (specification page 141). The specification is devoid of teaching of the number of samples tested, the statistical significance if any of the "more highly expressed" and the specific probe used for the alleged quantitative analysis performed. The data presented are not quantitative and as such, the relevance as compared to the recited control is ambiguous. Further, it appears that normal cells such as stomach and skin express the nucleic acid more highly as compared to tumors. As such, since the cDNA, proteins or antibodies are not described as being specifically correlated with a specific type of cancer the skilled artisan could not distinguish tumors from non-tumors based on the alleged "more highly expressed" criteria only. Therefore, the asserted use as diagnostic marker or targets of therapeutic intervention are not persuasive to impart a specific utility. This relevance of the asserted higher expression very vague, and does not disclose what mathematical calculations, if any, were used to establish significance of the finding across a variety of samples from different patients. Therefore, the apparent single data point presented in the quantitative PCR is preliminary at best, and cannot be evaluated or repeated independently

by the skilled artisan. Clearly, further research would be required of the skilled artisan to establish the statistical significance if any, and whether and how a probe used in the PCR assay could be used as diagnostic markers or therapeutic targets. Such further experimentation indicates that the asserted utility is not in currently available form for the disclosed nucleic acid of SEQ ID NO:37. Furthermore, the literature indicates that such results are to be evaluated very critically. For example, Hu et al. (2003, Journal of Proteome Research 2:405-412) analyzed 2286 genes that showed a greater than 1-fold difference in mean expression level between breast cancer samples and normal samples in a microarray (p. 408, middle of right column). Hu et al. discovered that, for genes displaying a 5-fold change or less in tumors compared to normal, there was no evidence of a correlation between altered gene expression and a known role in the disease. However, among genes with a 10-fold or more change in expression level, there was a strong and significant correlation between expression level and a published role in the disease (see discussion section). Therefore, in the absence of a statistical significance of the data and quantitative evaluation it would appear that the relationship between the reported "higher expression" as it relates to tumor formation and role in tumor formation or role in normal cells remains to be established. Consequently, any relevance with respct to using the nucleic acid, protein or antibody for therapeutic purposes remains to be established. With respect to the nucleic acids encoding the polypeptides, it is noted that the art establishes that increased mRNA production does not necessarily lead to increased protein production. Haynes et al. (Electrophoresis, 19:1862-1871, 1998) found "a general trend" but no significant correlation between nucleic acid level and translation and protein levels. Further, Haynes et al teach that polypeptide levels cannot be accurately predicted from mRNA levels and that variances as much as 40-fold or even 50-fold were not uncommon (p 1863). Haynes et al used yeast as an art-accepted model for eukaryotic systems. Further, the lack of demonstrable correlation of mRNA expression levels with protein levels was so well known in the art at the time of filing, it was reported in a general text

book. Lewin (Genes VI (1997) Chapter 29, pages 847-848) teaches that the concept that transcription levels do not correlate with protein levels was so well known to the art that it was presented in a textbook. Lewin, Genes VI (1997) Chapter 29, pages 847-848 which specifically teaches "... production of RNA cannot be inevitably be equated with production of protein...." (page 487, column 2, last paragraph . This concept reconfirmed by a variety of studies such as that evidenced by Gokman-Polar et al (Cancer Research 61:1375-1381, 2001) that indicates the absence of any necessary correlation between increased mRNA levels and increased protein levels. Gokman-Polar et al that teach "Quantitative reverse transcription-PCR analysis revealed that the PKC mRNA levels do not directly correlate with PKC protein levels, indicating that PKC isoenzyme expression is likely regulated at the posttranscriptional/translational level" (see abstract). Gokman-Polar et al show in Figure 6-7 that there is no increasing mRNA expression for any of the isoenzymes, while the protein is significantly overexpressed as shown by Figure 4-5. Anderson et al teach that "Despite extensive work on the regulation of many individual genes, little attention appears to have been paid to the global question of the relation between mRNA and corresponding cellular protein abundances.." (Anderson et al , Electrophoresis, 18:533-537, 1997; see page 536, column 2.). Anderson et al teach that the correlation is 0.48 and indicates that the two major phages of gene expression regulation are of approximately equal importance in determining the net output of protein. Reanalysis of the data of Kawamoto et al, indicates that the correlation is coefficient is poor when one gene product, well separated from the gene cluster is omitted from the calculation (Anderson et al page 536, column 2, first full paragraph). Further, the lack of correlation between mRNA levels and protein levels in cancer is demonstrated by Chen et al (Molecular and Cellular Proteomics, 1:304-313, April 2002). Chen et al indicate that "Using a quantitative analysis of mRNA and protein expression within the same lung adenocarcinomas, we showed that only a subset of the proteins exhibited a significant correlation with mRNA abundance." (see Chen et al page 304, column 1, abstract). As such, not all cancer protein have a correlation and

therefore, in the absence of any specific evidence to the contrary with respect to the polypeptide, variants thereof or antibodies that bind them, there is reason to doubt the asserted truth of the assertion of utility. Therefore, the skilled artisan immediately recognizes that, at the time of the invention, that no direct correlation between gene amplification/mRNA levels and increased polypeptide levels necessarily exists, no dogma exists between mRNA and polypeptide levels (for which neither are disclosed within the instant specification for polypeptide). Given the totality of the evidence provided by Haynes et al, Anderson et al, Chen et al and Lewin et al, it is clear that those skilled in the art would not assume that an alleged increase in gene copy number or increase in mRNA levels would correlate with increased polypeptide levels. One skilled in the art would have to do further research to determine whether or not the polypeptide levels were higher, and whether the higher levels were statistically significant. As such, the claimed nucleic acid encoding the protein does not have utility, because the protein *per se* has no utility.

Thus, the proposed use of the PRO1344 polynucleotides as diagnostic markers and therapeutic targets are simply starting points for further research and investigation into potential practical uses of the polynucleotides, encoded polypeptides and antibodies that bind the polypeptides. "The basic quid pro quo contemplated by the Constitution and the Congress for granting a patent monopoly is the benefit derived by the public from an invention with substantial utility", [u]nless and until a process is refined and developed to this point-where specific benefit exists in currently available form- there is insufficient justification for permitting an application to engross what may prove to be a broad filed", and "a patent is not a hunting license". "[i]t is not a reward for the search, but compensation for its successful conclusion." Similarly, the other listed and asserted utilities in the specification as exemplified by the other Examples are not particularly disclosed with respect to the claimed polynucleotide encoding a protein or are neither substantial nor specific due to being generic in nature and applicable to a myriad of such proteins. (*Brenner v. Manson*, 148 USPQ 689 (Sus. Ct. 1996). Additionally, the courts have

held that the disclosure is insufficient when testing is necessary to determine the actual use or possible lack of use (In re Kirk and Petrow (CCPA) 153 USPQ 48). Note, because the claimed invention is not supported by a specific and substantial asserted utility for the reasons set forth above, credibility has not been assessed. Neither the specification as filed nor any art of record discloses or suggests any property or activity for the nucleic acid per se, the polynucleic acid encoding the PRO polypeptide or the anti-PRO antibody that binds the polypeptide such that another non-asserted utility would be well established for the instantly claimed compounds.

Claim Rejections - 35 USC § 112

The following is a quotation of the first paragraph of 35 U.S.C. 112:
The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

The following is a quotation of the second paragraph of 35 U.S.C. 112:
The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1-20 are also rejected under 35 U.S.C. 112, first paragraph. Specifically, since the claimed invention is not supported by either a specific and substantial asserted utility or a well established utility for the reasons set forth above, one skilled in the art clearly would not know how to use the claimed invention.

Claims 1-6, 9, 10 and 14-20 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. This is a written description rejection.

The claims are drawn to nucleic acids encoding polypeptides having at least 80%, 85%, 90%, 95% or 99% sequence identity with a particular disclosed sequence or a sequence that hybridizes to a particular sequence. The claims are also drawn to fragments such as "the extracellular domain of a polypeptide lacking its associated signal peptide" or "the extracellular domain" of the polypeptide *per se*. The claims do not require that the nucleic acid possess any particular biological activity, nor any particular conserved structure, or other disclosed distinguishing feature. Thus, the claims are drawn to a genus of polypeptides that is defined only by sequence identity or undefined structure.

To provide adequate written description and evidence of possession of a claimed genus, the specification must provide sufficient distinguishing identifying characteristics of the genus. The factors to be considered include disclosure of complete or partial structure, physical and/or chemical properties, functional characteristics, structure/function correlation, methods of making the claimed product, or any combination thereof. In this case, the only factor present in the claim is a partial structure in the form of a recitation of percent identity or undefined fragment thereof. There is not even identification of any particular portion of the structure that must be conserved. Accordingly, in the absence of sufficient recitation of distinguishing identifying characteristics, the specification does not provide adequate written description of the claimed genus.

Vas-Cath Inc. v. Mahurkar, 19USPQ2d 1111, clearly states "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the 'written

description' inquiry, whatever is now claimed." (See page 1117.) The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed." (See Vas-Cath at page 1116). As discussed above, the skilled artisan cannot envision the detailed chemical structure of the encompassed genus of polynucleotides and encoded polypeptides, and therefore conception is not achieved until reduction to practice has occurred, regardless of the complexity or simplicity of the method of isolation. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method of isolating it. The compound itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601 at 1606 (CAFC 1993) and *Amgen Inc. v. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

One cannot describe what one has not conceived. See *Fiddes v. Baird*, 30 USPQ2d 1481 at 1483. In Fiddes, claims directed to mammalian FGF's were found to be unpatentable due to lack of written description for that broad class. The specification provided only the bovine sequence.

Further, the specification and Figure 38 in particular, does not teach the claimed extracellular domain structure of SEQ ID NO:38. The specification does not teach any subsequence of the polypeptide of SEQ ID NO:38 or Figure 38 that corresponds to an extracellular domain or extracellular domain lacking a signal sequence as recited in the claims. Therefore, the specification as filed does not set forth in a clear manner or in such a way as to reasonably convey to one skilled in the relevant art that the inventors, at the time the application was filed, had possession of the variants or fragments of the polypeptide as now claimed.

Therefore, only an isolated nucleic acid encoding a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:38, but not the full breadth of the claim meets the written description provision of 35 U.S.C. §112, first paragraph. Applicant is reminded that Vas-Cath makes clear that the written description provision of 35 U.S.C. §112 is severable from its enablement provision (see page 1115).

Claims 1-6 and 13-20 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the enablement requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to enable one skilled in the art to which it pertains, or with which it is most nearly connected, to make and/or use the invention.

The specification at pages 120-123 lacks complete deposit information for the deposit of the full length cDNA encoding the claimed polypeptide deposited at the American Type Culture Collection as set forth in embodiment (e) of claims 1-6, 13, 14 and claims 15-20 as dependent there from. It is not clear that the deposit is known and publicly available or can be reproducibly isolated from nature without undue experimentation or if it is the same as SEQ ID NO:37 encoding the polypeptide of SEQ ID NO:38 or contains additional nucleic acid sequences that encode additional amino acid residues. As such, a deposit for patent purposes is required. The referral to the deposit on page 123 is an insufficient assurance that all required deposits have been made and all the conditions of 37 CFR 1.801-1.809 have been met. The specification states that pursuant to an "agreement" between Genentech, Inc. and the ATCC™, permanent unrestricted availability to the public of the progeny of the culture upon issuance of "the pertinent US Patent" is provided for. This is insufficient because agreements are contracts that are revocable and the conditions therein are revocable. Further, it is unclear what would be considered the "pertinent US Patent". As such, Applicants are required to provide assurances that All restrictions upon pubic access to the ATCC™ accession number 203133 as specifically claimed, will be "irrevocably removed upon the grant of a patent from this application" specifically using this exact language. Since "agreements" are subject to revocation, this assurance is required for patent purposes. The assurances should be made by an affidavit or declaration by Applicants or Assignees or a statement by an attorney of record who has authority and control over conditions of the deposit over his or her signature and registration number. Applicants are specifically

directed to MPEP 2424.01 that states "with one possible exception (37 CFR 1.808(b)), that all restrictions on the accessibility be irrevocably removed by the applicant upon the granting of the patent" are required see *Ex parte Hildebrand*, 15 USPQ2d 1662 (Bd. Pat. App. & Int. 1990). Further, the statement is not in compliance with MPEP 1.806 that requires "A deposit made before or during pendency of an application for patent shall be made for a term of at least thirty (30) years and at least five (5) years after the most recent request for the furnishing of a sample of the deposit was received by the depository. In any case, samples must be stored under agreements that would make them available beyond the enforceable life of the patent for which the deposit was made."

Claims 1-6, 9, 10, 14-20 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

As to all of the recited claims. The claims comprise the limitations that the claimed nucleic acid encoding the polypeptide comprise an "extracellular domain" or "the extracellular domain lacking its associated signal peptide", and "the extracellular domain" is not defined in the specification or claims. These limitations are indefinite because neither the figure nor the specification define or teach the metes and bounds of these specific fragments. Further, if the protein has an extracellular domain, the recitation of "the extracellular domain"..."lacking its associated signal sequence" is indefinite as a signal sequence is not generally considered to be part of an extracellular domain, as signal sequences are cleaved from said domains in the process of protein production in the cell.

Additionally, claim 15 recites "hybridization under stringent conditions". Neither the specification nor the art define these conditions unambiguously. Therefore, the skilled artisan would be unable to determine the metes and bounds of the claimed invention in the absence of a recitation of clear, definite hybridization conditions in the claims.

Claim Rejections - 35 USC § 102

The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless -

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

(e) the invention was described in a patent granted on an application for patent by another filed in the United States before the invention thereof by the applicant for patent, or on an international application by another who has fulfilled the requirements of paragraphs (1), (2), and (4) of section 371(c) of this title before the invention thereof by the applicant for patent.

Claims 1-20 are rejected under 35 U.S.C. 102(b) as being anticipated by Baker et al (WO 99/63088, published 12-9-99).

Baker et al teach a nucleic acid that is 100% identical as compared to SEQ ID NO:37 and encodes a polypeptide of SEQ ID NO:38 (see attached alignment). Baker et al teach the mature protein lacking the signal sequence (see pages 147-149). Baker et al teach the nucleic acid in an expression vector and the expression vector in a suitable host cell such as E. coli, yeast or CHO cells (see pages 352-355). As such Baker et al anticipates the instantly claimed invention.

Claims 1-6, 9, 10 and 14-20 are rejected under 35 U.S.C. 102(b) as being anticipated by Barnes et al (WO 00/18904, published 06 April 2000).

Barnes et al teach a nucleic acid encoding a protein named Tango 215. The nucleic acid of Barnes et al is 99% identical as compared with SEQ ID NO:37 and encodes a polypeptide that is 99.8% identical as compared with SEQ ID NO:38 (see attached alignments). Barnes et al teach the mature polypeptide (i.e. lacking the signal sequence at page 46). Barns et al teach expression vectors and host cells comprising the expression vectors. Barns et al teach *E. coli* , yeast cells and mammalian cells as host cells for recombinant production of the encoded protein (see page 5, lines 10-19; page 76-83). Barnes et al teach nucleic acids that hybridize to the nucleic acids described therein under standard conditions and fragmetns thereof (see page 49, lines 14-29 and page 53). In the absence of a defined extracellular domain in the specification and the claims, the nucleic acid of the prior art is deemed 100% identical to an extracellular portion of the claimed nucleic acid and as such meets the markush members (c-d) of claims 1-6, 14-16 and dependent claims 9, 10 and 17-20. Further, the prior art meets claims 1-5 as it anticipates embodiments (a, b, e, f and g).

Claims 14-16 are rejected under 35 U.S.C. 102(e) as being clearly anticipated by Robinson et al (US Patent No. 6,331,427 issued 12-18-01, filed March 26, 1999).

Robinson et al teach SEQ ID NO:179. SEQ ID NO:179 is 99.8% similar to residues 381-800 of SEQ ID NO:37 (see attached alignment). The sequences have more than 100 consecutive nucleotide residues that are identical. Therefore, the sequence of the prior art would inherently hybridize to SEQ ID NO:37 or any of the nucleic acids encoding SEQ ID NO:38.

Since the Office does not have the facilities for examining and comparing applicant's nucleic acid with that of the prior art, the burden is on applicant to show a novel or unobvious difference between the claimed product and the product of the prior art (i.e., that the nucleic acid of the prior art does not possess the same functional

characteristics of the claimed nucleic acid). See *In re Best*, 562 F.2d 1252, 195 USPQ 430 (CCPA 1977) and *In re Fitzgerald* et al., 619 F.2d 67, 205 USPQ 594 (CCPA 1980).

Status of the Claims

Claims 1-20 stand rejected.

Conclusion

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Patricia A. Duffy whose telephone number is 571-272-0855. The examiner can normally be reached on M-Th 6:30 am - 6:00 pm. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lynette Smith can be reached on 571-272-0864.

The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Patricia A. Duffy, Ph.D.
Primary Examiner
Art Unit 1645

Duffy, Patricia

From: Duffy, Patricia
Sent: Monday, August 16, 2004 6:22 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search 10/063692

Importance: High

In re:10/063,692

Please search SEQ ID NOs:38 and 37 and oligomers thereof.
Please run the amino acid sequence of SEQ ID NO:38 against the NA database.
Please perform a commercial and interference database search.

Please print out top 100 hits in each of the above.

Thank you.

Patricia A. Duffy, Ph.D.
Art Unit 1645, Remsen 3B05
571-272-0855

Ex Notes

FIGURE 38

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKREVVGYT
IPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQ
VLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQII
KRVCGNERPAPIQSIGSSLHVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKC
ACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTVVSFFCNNSYVLSGNE
KRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTK
KPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPSCIPICGKIENITAP
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DLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCA
SWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWI
ERNMK

Important features of the protein:

Signal peptide:
amino acids 1-23

EGF-like domain cysteine pattern signature.
amino acids 260-272

N-glycosylation sites.
amino acids 96-100, 279-283, 316-320, 451-455, 614-618

N-myristoylation sites.
amino acids 35-41, 97-103, 256-262, 284-290, 298-304, 308-314, 474-480, 491-497, 638-644, 666-672

Amidation site.
amino acids 56-60

Serine proteases, trypsin family.
amino acids 489-506

CUB domain proteins profile.
amino acids 150-167

PD extracellular domain

FIGURE 37

CGCTCGGGCACCAGCCGCGGCAAGG<u>ATG</u>GAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCTCCTTCTCATC
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> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-063-692-37.res made by tport on Thu 14 Jul 105 11:38:51-PST.

Query sequence being compared:US-10-063-692-37 (1-2846)
Number of sequences searched:                   3
Number of scores above cutoff:                  3

      Results of the initial comparison of US-10-063-692-37 (1-2846) with:
        File : aaa39951.seq
        File : aaz65034.seq
        File : abk30334.seq

    100-
       -
N      -
U   50-
M      -
B      -
E      -
R      -
       -
O      -
F   10-
       -
S      -
E    5-
Q      -
U      -
E      -
N      -
C      -
E      -                    *                                      * *
S    0-------------------------------------------------------------------
       |     |     ||     |     |     |     | |    |     |     |    | |
SCORE  0    316   632|   949   1265  1581  |1897  2214  2530  2846
STDEV               -1                     0                    1

                              PARAMETERS

Similarity matrix      Unitary    K-tuple                  4
Mismatch penalty             1    Joining penalty         30
Gap penalty               5.00    Window size            500
Gap size penalty          0.33
Cutoff score                 1
Randomization group          0

                          SEARCH STATISTICS

Scores:                   Mean      Median      Standard Deviation
                          2189      993         1038.28

Times:                    CPU                   Total Elapsed
                     00:00:00.00                00:00:00.00

Number of residues:                   8479
Number of sequences searched:            3
Number of scores above cutoff:           3

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:
                                                      Init. Opt.
Sequence Name    Description                   Length Score Score  Sig. Frame
------------------------------------------------------------------------------
  1. aaz65034     Membrane-bound protein PRO134   2846  2846  2846   0.63    0

The list of other best scores is:
                                                      Init. Opt.
Sequence Name    Description                   Length Score Score  Sig. Frame
------------------------------------------------------------------------------
  2. aaa39951     Human TANGO 215 cDNA.           2747  2729  2729   0.52    0
           ****  1 standard deviation below mean ****
  3. abk30334     Human G-protein-coupled prote   2886   992  2506  -1.15    0

1. US-10-063-692-37 (1-2846)
   aaz65034      Membrane-bound protein PRO1344 encoding cDNA.

Initial Score     =   2846  Optimized Score  =    2846  Significance =  0.63
Residue Identity =    100%  Matches          =    2846  Mismatches   =     0
Gaps              =      0  Conservative Substitutions             =     0

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       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       CGCTCGGGCACCAGCCGCGGCAAGGATGGAGCTGGGTTGCTGGACGCAGTTGGGGCTCACTTTTCTTCAGCT
       X        10        20        30        40        50        60        70

              80        90       100       110       120       130       140
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       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       CCTTCTCATCTCGTCCTTGCCAAGAGAGTACACAGTCATTAATGAAGCCTGCCCTGGAGCAGAGTGGAATAT
              80        90       100       110       120       130       140

            150       160       170       180       190       200       210
       CATGTGTCGGGAGTGCTGTGAATATGATCAGATTGAGTGCGTCTGCCCCGGAAAGAGGGAAGTCGTGGGTTA
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       CATGTGTCGGGAGTGCTGTGAATATGATCAGATTGAGTGCGTCTGCCCCGGAAAGAGGGAAGTCGTGGGTTA
            150       160       170       180       190       200       210

          220       230       240       250       260       270       280
       TACCATCCCTTGCTGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       TACCATCCCTTGCTGCAGGAATGAGGAGAATGAGTGTGACTCCTGCCTGATCCACCCAGGTTGTACCATCTT
          220       230       240       250       260       270       280

     290       300       310       320       330       340       350       360
       TGAAAACTGCAAGAGCTGCCGAAATGGCTCATGGGGGGGTACCTTGGATGACTTCTATGTGAAGGGGTTCTA
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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              370       380       390       400       410       420       430
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       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       CTGTGCAGAGTGCCGAGCAGGCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAA
              370       380       390       400       410       420       430

             440       450       460       470       480       490       500
       GGGTCAGATTTTGTTGGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       GGGTCAGATTTTGTTGGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTT
             440       450       460       470       480       490       500

            510       520       530       540       550       560       570
       TGTCATCCAACTAAGATTTGTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGTATGACTATGTTGAGGT
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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            510       520       530       540       550       560       570

           580       590       600       610       620       630       640
       TCGTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAGCGGCCAGCTCCTATCCA
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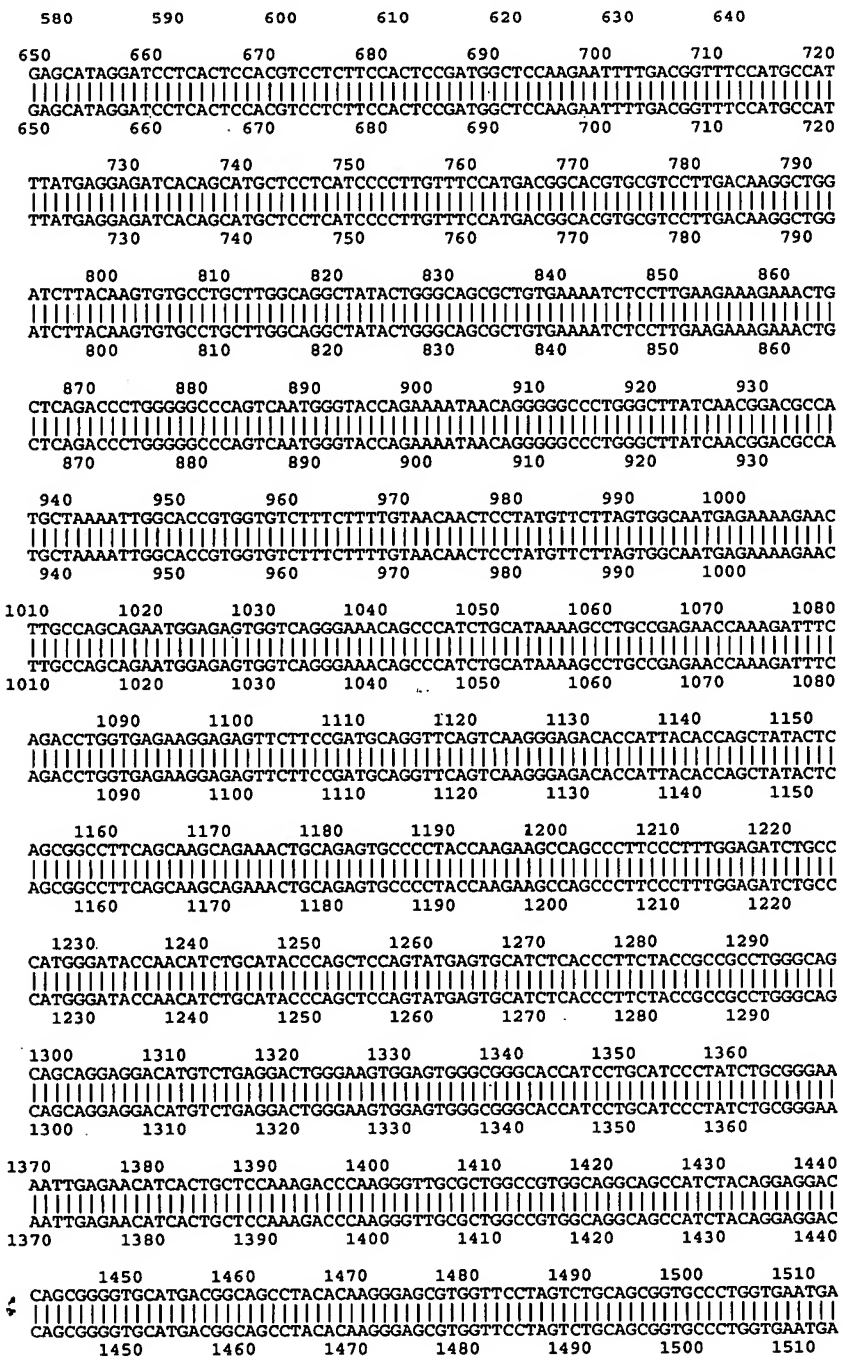
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800 810 820 830 840 850 860
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870 880 890 900 910 920 930
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CTCAGACCCTGGGGGCCCAGTCAATGGGTACCAGAAAATAACAGGGGGCCCTGGGCTTATCAACGGACGCCA
870 880 890 900 910 920 930
940 950 960 970 980 990 1000
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1230 1240 1250 1260 1270 1280 1290
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1370 1380 1390 1400 1410 1420 1430 1440
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1450 1460 1470 1480 1490 1500 1510
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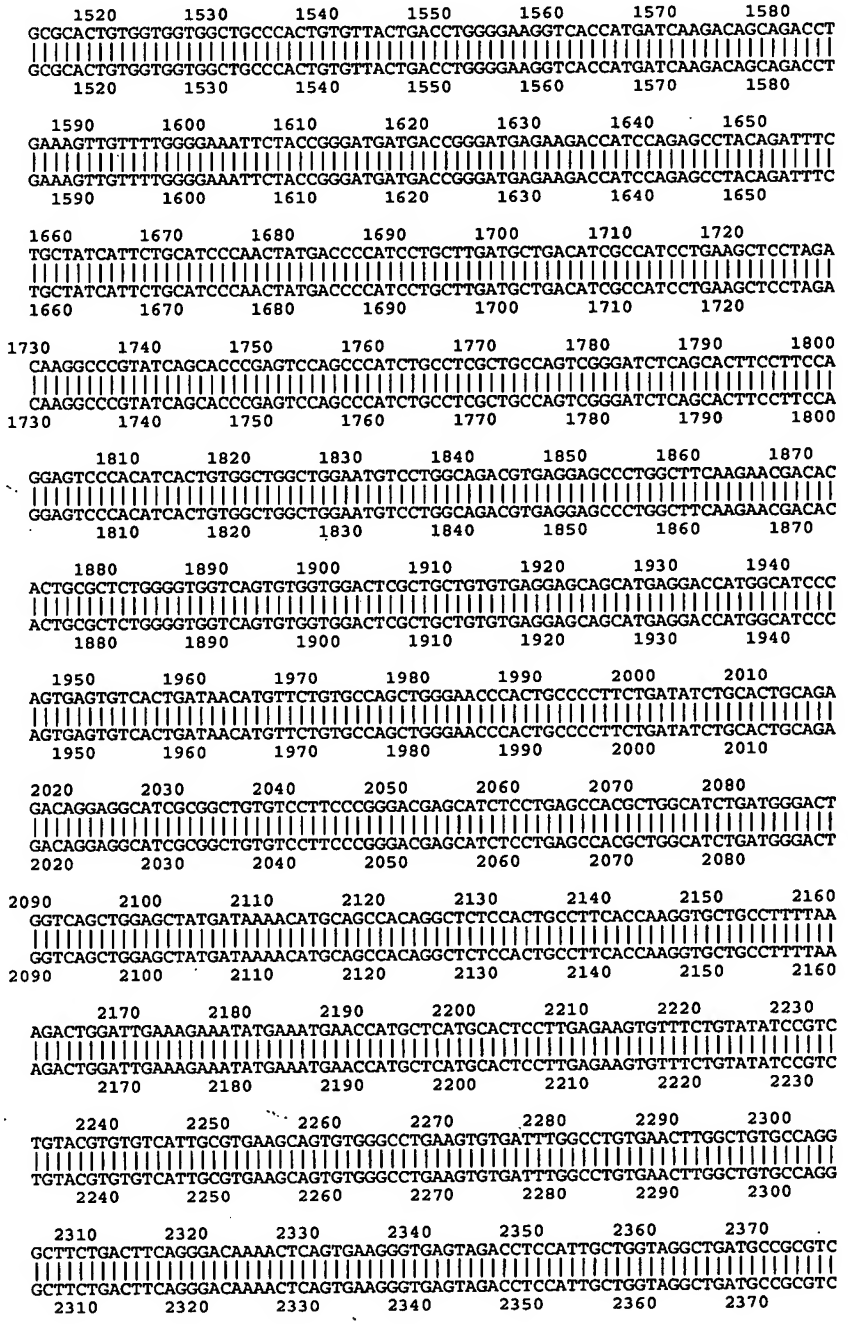
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1950 1960 1970 1980 1990 2000 2010
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2020 2030 2040 2050 2060 2070 2080
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2310 2320 2330 2340 2350 2360 2370
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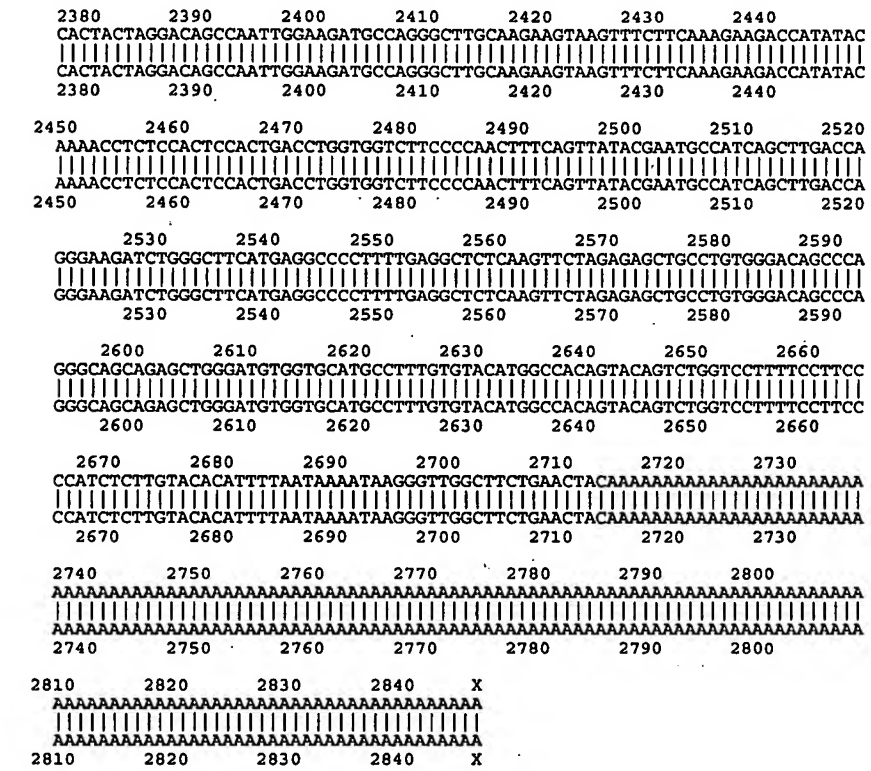
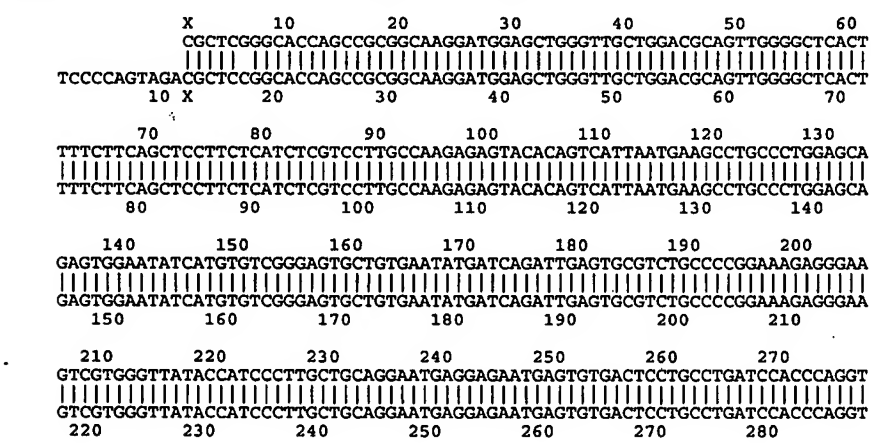
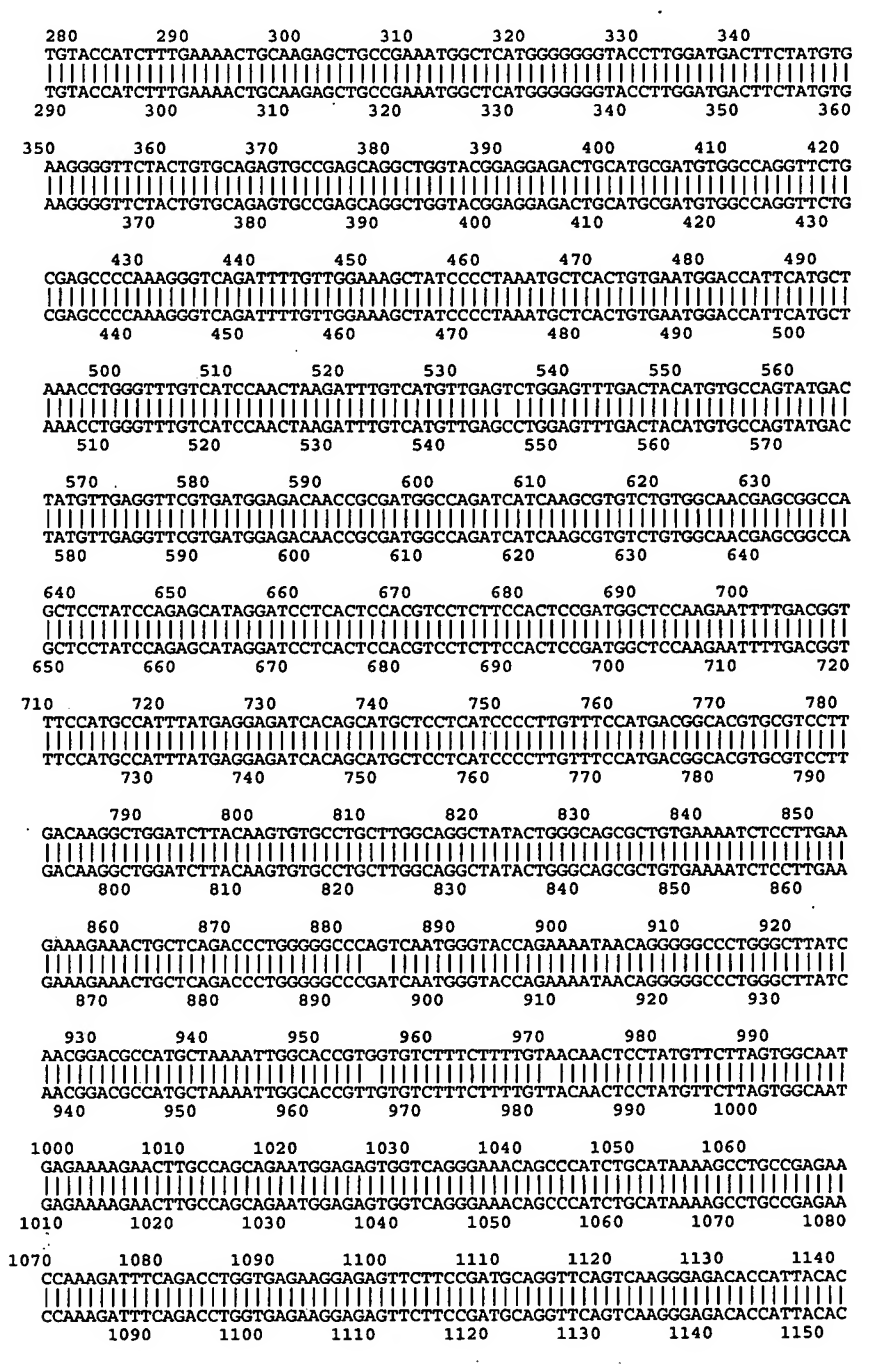
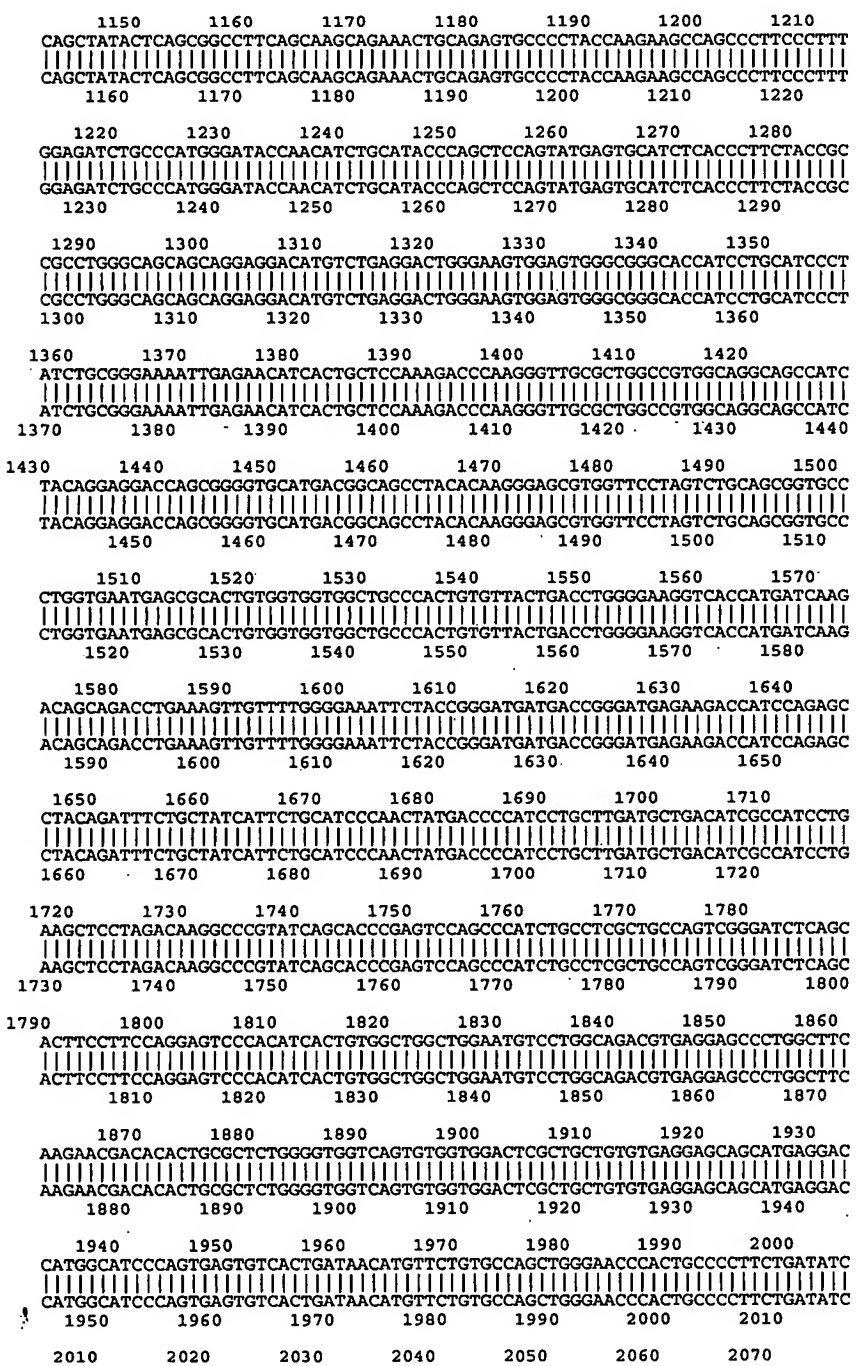


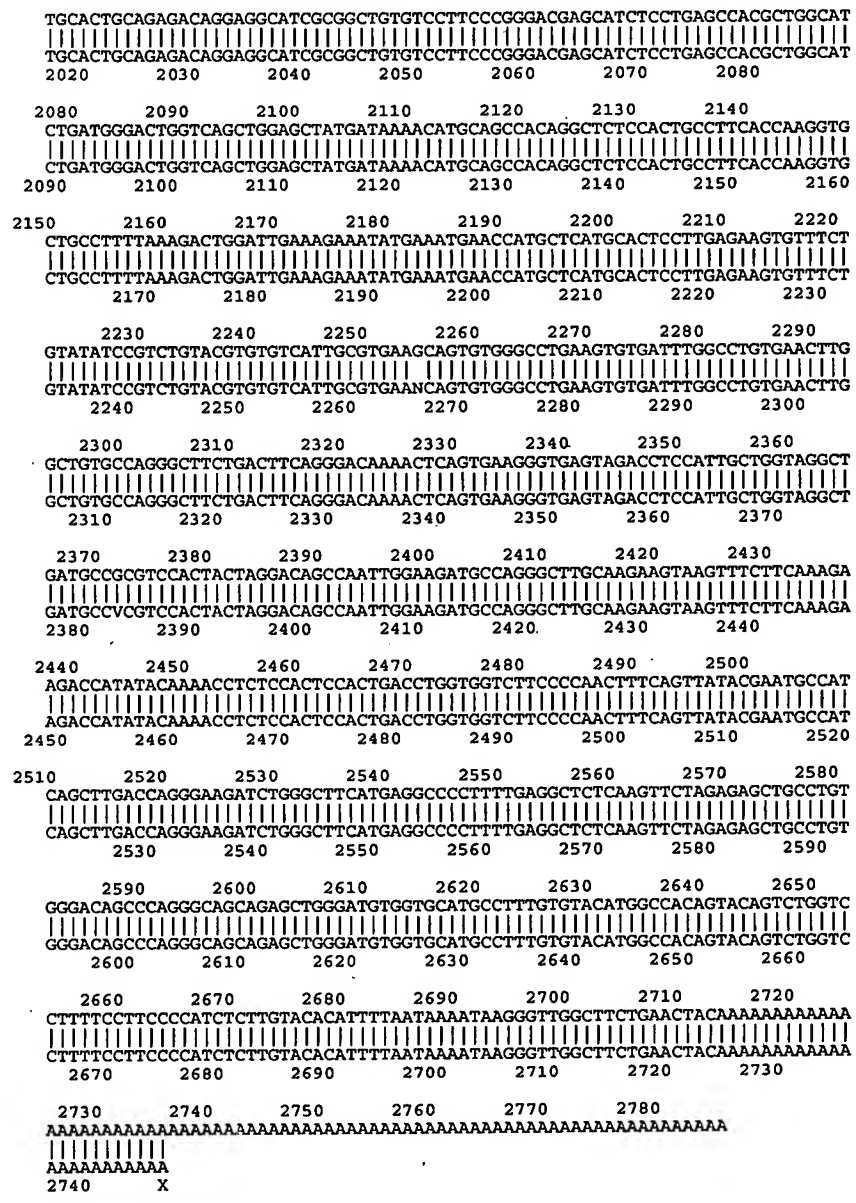
2. US-10-063-692-37 (1-2846)
aaa39951 Human TANGO 215 cDNA.

Initial Score = 2729 Optimized Score = 2729 Significance = 0.52
Residue Identity = 99% Matches = 2729 Mismatches = 7
Gaps = 0 Conservative Substitutions = 0



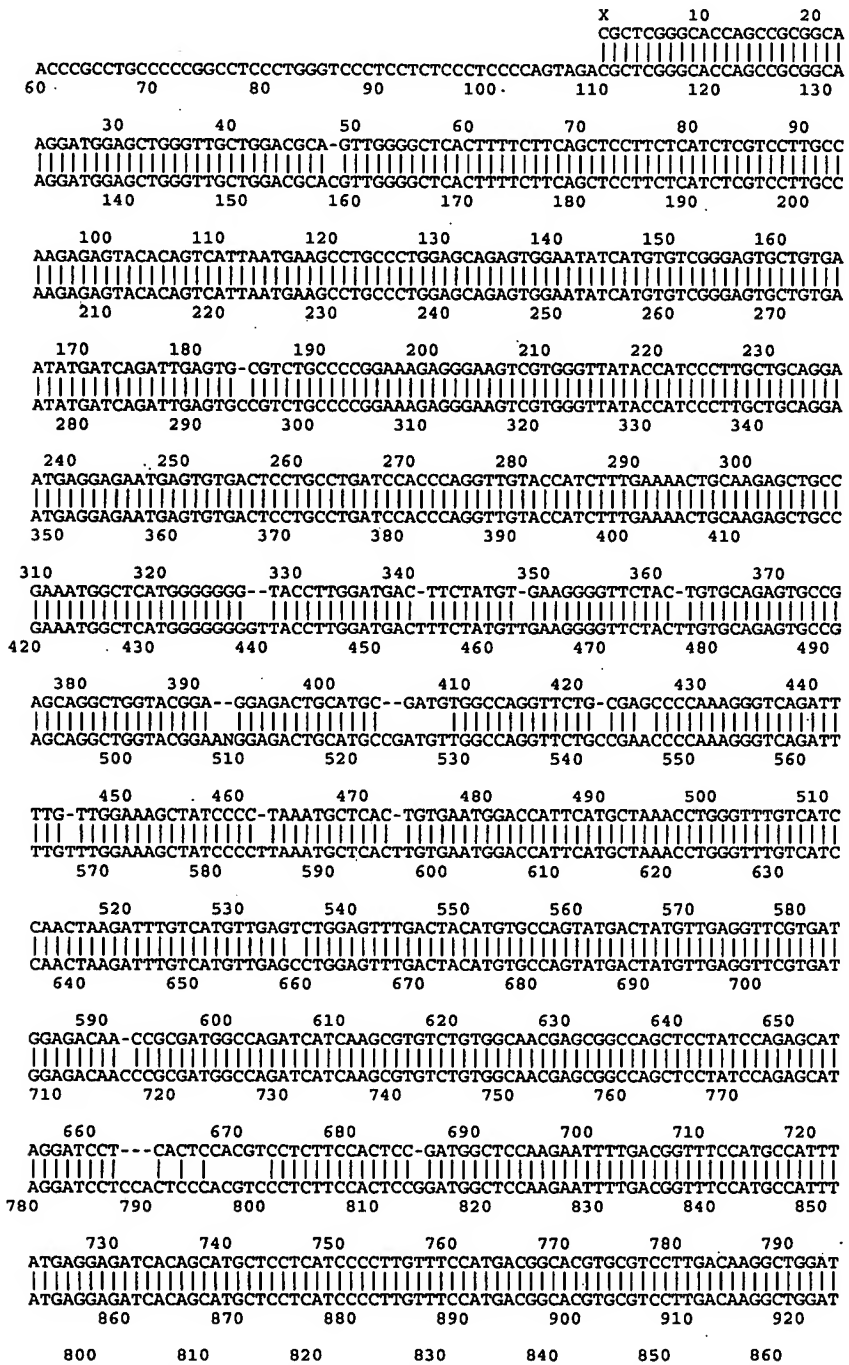


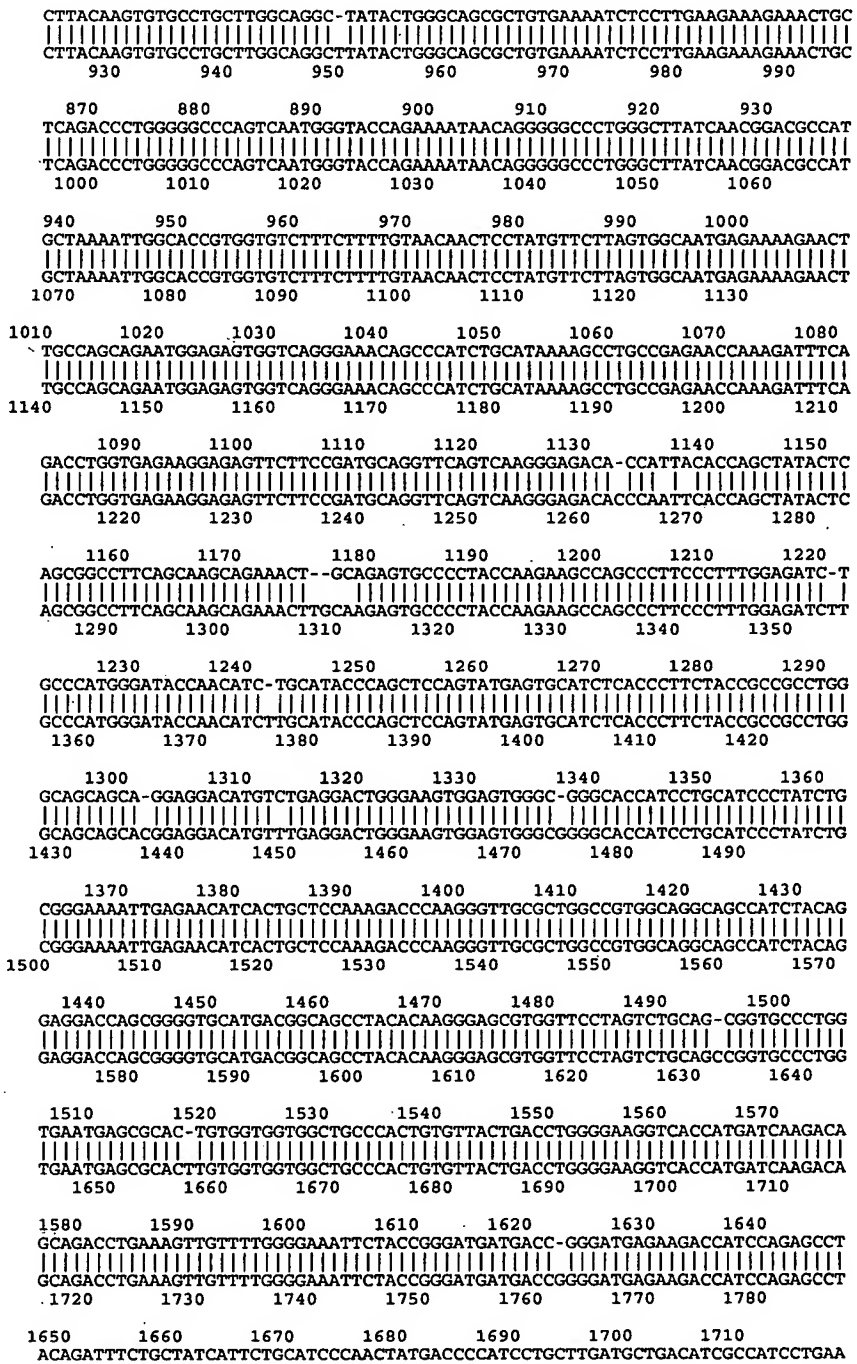


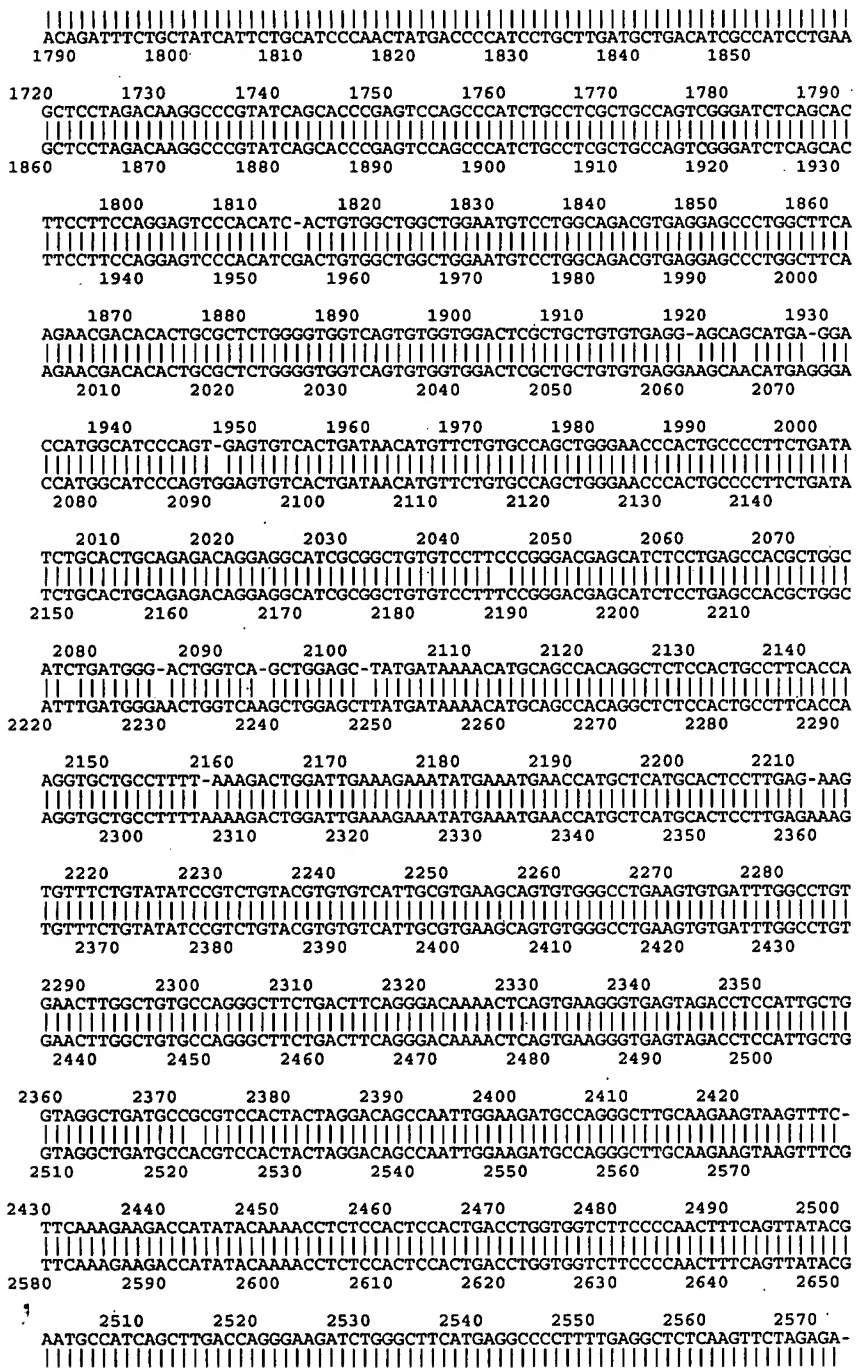


3. US-10-063-692-37 (1-2846)
abk30334 Human G-protein-coupled protease #104.

Initial Score	=	992	Optimized Score	=	2506	Significance	= -1.15
Residue Identity	=	97%	Matches	=	2699	Mismatches	= 33
Gaps	=	45	Conservative Substitutions				= 0



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1790 1800 1810 1820 1830 1840 1850
1720 1730 1740 1750 1760 1770 1780 1790
GCTCCTAGACAAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAGTCGGGATCTCAGCAC
GCTCCTAGACAAGGCCCGTATCAGCACCCGAGTCCAGCCCATCTGCCTCGCTGCCAGTCGGGATCTCAGCAC
1860 1870 1880 1890 1900 1910 1920 1930
1800 1810 1820 1830 1840 1850 1860
TTCCTTCCAGGAGTCCCACATC-ACTGTGGCTGGCTGGAATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCA
TTCCTTCCAGGAGTCCCACATCGACTGTGGCTGGCTGGAATGTCCTGGCAGACGTGAGGAGCCCTGGCTTCA
1940 1950 1960 1970 1980 1990 2000
1870 1880 1890 1900 1910 1920 1930
AGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGG-AGCAGCATGA-GGA
AGAACGACACACTGCGCTCTGGGGTGGTCAGTGTGGTGGACTCGCTGCTGTGTGAGGAAGCAACATGAGGGA
2010 2020 2030 2040 2050 2060 2070
1940 1950 1960 1970 1980 1990 2000
CCATGGCATCCCAGT-GAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCCTTCTGATA
CCATGGCATCCCAGTGGAGTGTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCCTTCTGATA
2080 2090 2100 2110 2120 2130 2140
2010 2020 2030 2040 2050 2060 2070
TCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGTCCTTCCCGGGACGAGCATCTCCTGAGCCACGCTGGC
TCTGCACTGCAGAGACAGGAGGCATCGCGGCTGTGTCCTTTCCGGGACGAGCATCTCCTGAGCCACGCTGGC
2150 2160 2170 2180 2190 2200 2210
2080 2090 2100 2110 2120 2130 2140
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ATTTGATGGGAACTGGTCAAGCTGGAGCTTATGATAAAACATGCAGCCACAGGCTCTCCACTGCCTTCACCA
2220 2230 2240 2250 2260 2270 2280 2290
2150 2160 2170 2180 2190 2200 2210
AGGTGCTGCCTTTT-AAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAG-AAG
AGGTGCTGCCTTTTAAAAGACTGGATTGAAAGAAATATGAAATGAACCATGCTCATGCACTCCTTGAGAAAG
2300 2310 2320 2330 2340 2350 2360
2220 2230 2240 2250 2260 2270 2280
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCCTGAAGTGTGATTTGGCCTGT
TGTTTCTGTATATCCGTCTGTACGTGTGTCATTGCGTGAAGCAGTGTGGGCCTGAAGTGTGATTTGGCCTGT
2370 2380 2390 2400 2410 2420 2430
2290 2300 2310 2320 2330 2340 2350
GAACTTGGCTGTGCCAGGGCTTCTGACTTCAGGGACAAAACTCAGTGAAGGGTGAGTAGACCTCCATTGCTG
GAACTTGGCTGTGCCAGGGCTTCTGACTTCAGGGACAAAACTCAGTGAAGGGTGAGTAGACCTCCATTGCTG
2440 2450 2460 2470 2480 2490 2500
2360 2370 2380 2390 2400 2410 2420
GTAGGCTGATGCCGCGTCCACTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTC-
GTAGGCTGATGCCACGTCCACTACTAGGACAGCCAATTGGAAGATGCCAGGGCTTGCAAGAAGTAAGTTTCG
2510 2520 2530 2540 2550 2560 2570
2430 2440 2450 2460 2470 2480 2490 2500
TTCAAAGAAGACCATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCCAACTTTCAGTTATACG
TTCAAAGAAGACCATATACAAAACCTCTCCACTCCACTGACCTGGTGGTCTTCCCCAACTTTCAGTTATACG
2580 2590 2600 2610 2620 2630 2640 2650
2510 2520 2530 2540 2550 2560 2570
AATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAGGCCCCTTTTGAGGCTCTCAAGTTCTAGAGA-


AATGCCATCAGCTTGACCAGGGAAGATCTGGGCTTCATGAGGCCCCTTTTGAGGCTCTCAAGTTCTAGAGAC
2660 2670 2680 2690 2700 2710 2720
2580 2590 2600 2610 2620 2630 2640
GCTGCCTGTGGGACAGCCCAGGGCAGCAGAGCTGGGA--TGTGGTGCATGCCTTTGTGTACATGGCCACAGT
GCTGCCTGTGGGACAGCCCAGGGCAGCAGAGCTGGGAATTGTGGTGCATGCCTTTGTGTACATGGCCACAGT
2730 2740 2750 2760 2770 2780 2790
2650 2660 2670 2680 2690 2700 2710
AC-AGTCTGGTCCTTTTCCTTCCCCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTCTGAACTAC
ACAAGTCTGGTCCTTTTCCTTCCCCATCTCTTGTACACATTTTAATAAAATAAAGGGTTGGCTTCTGACTAC
2800 2810 2820 2830 2840 2850 2860
2720 2730 X 2740 2750 2760 2770 2780
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAGG
2870 2880 X

```
> O <
O| |O  IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-10-063-692-38.res made by tport on Thu 14 Jul 105 11:41:34-PST.


Query sequence being compared:US-10-063-692-38 (1-720)
Number of sequences searched:                  2
Number of scores above cutoff:                 2

      Results of the initial comparison of US-10-063-692-38 (1-720) with:
        File : aaa39951.pep
        File : aay88280.pep
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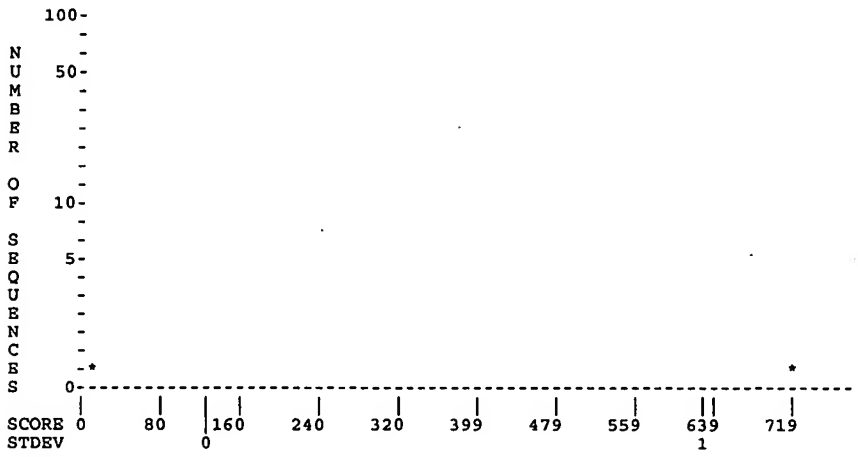


```
                              PARAMETERS

Similarity matrix       PAM-150     K-tuple                      1
Threshold level of sim.     16%
Mismatch penalty              1     Joining penalty             20
Gap penalty                5.00     Window size                500
Gap size penalty           0.05
Cutoff score                  1
Randomization group           0

                          SEARCH STATISTICS

Scores:                    Mean       Median     Standard Deviation
                            368           19          495.68

Times:                      CPU                    Total Elapsed
                       00:00:00.00                 00:00:00.00

Number of residues:                    962
Number of sequences searched:            2
Number of scores above cutoff:           2


The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.
```

The list of best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. aay88280	Human TANGO 215 protein.	720	719	719	0.71	0
2. aaa39951	TOIG of: aaa39951 check: 738	242	18	107	-0.71	0

1. US-10-063-692-38 (1-720)
   aay88280 Human TANGO 215 protein.

```
Initial Score    =    719  Optimized Score  =    719  Significance =  0.71
Residue Identity =    99%  Matches          =    718  Mismatches   =     1
Gaps             =      0  Conservative Substitutions               =     1

    X       10        20        30        40        50        60        70
    MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKREVVGYTIPCCRNE
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKREVVGYTIPCCRNE
    X       10        20        30        40        50        60        70

          80        90       100       110       120       130       140
    ENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQVLRAPKGQILLESY
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    ENECDSCLIHPGCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQVLRAPKGQILLESY
          80        90       100       110       120       130       140

       150       160       170       180       190       200       210
    PLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHV
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    PLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHV
       150       160       170       180       190       200       210

     220       230       240       250       260       270       280
    LFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVN
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|
    LFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPIN
     220       230       240       250       260       270       280

290       300       310       320       330       340       350       360
    GYQKITGGPGLINGRHAKIGTVVSFPCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
    |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
    GYQKITGGPGLINGRHAKIGTVVSFFCYNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVL
290       300       310       320       330       340       350       360

       370       380       390       400       410       420       430
    PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRT
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    PMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRT
       370       380       390       400       410       420       430

     440       450       460       470       480       490       500
    GKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAH
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    GKWSGRAPSCIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNERTVVVAAH
     440       450       460       470       480       490       500

       510       520       530       540       550       560       570
    CVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARISTRV
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    CVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARISTRV
       510       520       530       540       550       560       570

     580       590       600       610       620       630       640
    QPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVVSVVDSLLCEEQHEDHGIPVSVTDNMF
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
    QPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTLRSGVVSVVDSLLCEEQHEDHGIPVSVTDNMF
     580       590       600       610       620       630       640

   650       660       670       680       690       700       710         X
    CASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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  CASWEPTAPSDICTAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK
 650       660       670       680       690       700       710       720

2. US-10-063-692-38 (1-720)
   aaa39951     TOIG of: aaa39951  check: 7384  from: 1  to: 242

Initial Score    =    18  Optimized Score  =    107  Significance = -0.71
Residue Identity =   10%  Matches          =     34  Mismatches   =   188
Gaps             =    88  Conservative Substitutions              =    20

          20        30        40        50        60 X      70        80
  TFLQLLLISSLPREYTVINEACPGAEWNIMCRECCEYDQIECVCPGKREVVGYTIPCCRNEENECDSCLIHP
                                                      |    | |       : |:
                                                     MGLLECCARCLVGAPFASLVAT
                                                     X       10        20

        90       100       110       120       130       140       150
  GCTIFENCKSCRNGSWGGTLDDFYVKGFYCAECRAGWYGGDCMRCGQVLRAPKGQILLESYPLNAHCEWTIH
  |   |     |  |  : |  :  :  ::          |        |        :       |
  GLCFFGVALFCGCGHEALTGTEKLIETYFSKNYQDYEYLINVIHAFQYVIYGTASFFFLYGAL---------
        30        40        50        60        70        80

     160       170       180       190       200       210       220
  AKPGFVIQLRFVMLSLEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSLHVLFHSDGSKNFD
                    :    :          |       :||     |    |   :| |        :
  -------------------LLAEGFYTTGAVRQIFGDYKTTICGKGLSATFVGITYALTVVWLLVFACSAV
                          90        100       110       120       130

     230       240       250       260       270       280       290
  GFHAIYEEITACSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEERNCSDPGGPVNGYQKITGGPGL
      :    | | |
  PVYIYFNTWTTCQSI---------------------------------------------------------
  140       150

 300       310       320       330       340       350       360       370
  INGRHAKIGTVVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMQVQSRETPL
    :  :|   :   |  :              |    ||  |            :   |
  --AFPSKTSASIGSLCADARMYGVLPWNAFPGKVCGSNLLSICKTAEFQMTFHLFIAAFVGAAATLVSLLTF
       160       170       180       190       200       210       220

       380       390       400       410       420       430       440
  HQLYSAAFSKQKLQSAPTKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS
          |:  ||     ||
  MIAATYNPAVLKLMGRGTKF
       230       240 X
```

```
Qy       2466 CTGACCTGGTGGTCTTCCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAA 2525
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1991 CTGACCTGGTGGTCTTCCCCAACTTTCAGTTATACGAATGCCATCAGCTTGACCAGGGAA 2050

Qy       2526 GATCTGGGCTTCATGAGGCCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGA 2585
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2051 GATCTGGGCTTCATGAGGCCCCTTTTGAGGCTCTCAAGTTCTAGAGAGCTGCCTGTGGGA 2110

Qy       2586 CAGCCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTTTGTGTACATGGCCACAGTACA 2645
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2111 CAGCCCAGGGCAGCAGAGCTGGGATGTGGTGCATGCCTTTGTGTACATGGCCACAGTACA 2170

Qy       2646 GTCTGGTCCTTTTCCTTCCCCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTC 2705
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2171 GTCTGGTCCTTTTCCTTCCCCATCTCTTGTACACATTTTAATAAAATAAGGGTTGGCTTC 2230

Qy       2706 TGAACTACAAAAAAAAAAAAAAAAAAAAA 2734
             |||||||||||||||||||||||||||||
Db       2231 TGAACTACAAAAAAAAAAAAAAAAAAAAA 2259


RESULT 4
US-09-280-116-179
; Sequence 179, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
;  FILE REFERENCE: 5800-24, 035800/176965
;  CURRENT APPLICATION NUMBER: US/09/280,116A
;  CURRENT FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
;   LENGTH: 505
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: asticin/m 12a metalloproteases
US-09-280-116-179

  Query Match             13.0%;  Score 370;  DB 3;  Length 505;
  Best Local Similarity   99.8%;  Pred. No. 5.8e-134;
  Matches  420;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        381 GCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGTCAGA 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 GCTGGTACGGAGGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGTCAGA 110

Qy        441 TTTTGTTGGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTG 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 TTTTGTTGGAAAGCTATCCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTG 170

Qy        501 GGTTTGTCATCCAACTAAGATTTGTCATGTTGAGTCTGGAGTTTGACTACATGTGCCAGT 560
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        171 GGTTTGTCATCCAACTAAGATTTGTCATGTTGAGCCTGGAGTTTGACTACATGTGCCAGT 230

Qy        561 ATGACTATGTTGAGGTTCGTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCT 620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 ATGACTATGTTGAGGTTCGTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCT 290

Qy        621 GTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCACGTCCTCTTCC 680
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 GTGGCAACGAGCGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCACGTCCTCTTCC 350

Qy        681 ACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT 740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 ACTCCGATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCAT 410

Qy        741 GCTCCTCATCCCCTTGTTTCCATGACGGCACGTGCGTCCTTGACAAGGCTGGATCTTACA 800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GCTCCTCATCCCCTTGTTTCCATGACGGCACGTGCGTCCTTGACAAGGCTGGATCTTACA 470

Qy        801 A 801
              |
Db        471 A 471


RESULT 5
US-09-280-116-104
; Sequence 104, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
;  FILE REFERENCE: 5800-24, 035800/176965
;  CURRENT APPLICATION NUMBER: US/09/280,116A
;  CURRENT FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 104
;   LENGTH: 2886
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: trypsin-like serine proteases
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(2886)
;   OTHER INFORMATION: n = a, t, c or g
US-09-280-116-104

  Query Match             11.6%;  Score 329;  DB 3;  Length 2886;
  Best Local Similarity   99.8%;  Pred. No. 3.6e-118;
  Matches  449;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        686 GATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCC 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        815 GATGGCTCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCC 874

Qy        746 TCATCCCCTTGTTTCCATGACGGCACGTGCGTCCTTGACAAGGCTGGATCTTACAAGTGT 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        875 TCATCCCCTTGTTTCCATGACGGCACGTGCGTCCTTGACAAGGCTGGATCTTACAAGTGT 934

Qy        806 GCCTGCTTGGCAGGC-TATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAAACTG 864
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        935 GCCTGCTTGGCAGGCTTATACTGGGCAGCGCTGTGAAAATCTCCTTGAAGAAAGAAACTG 994

Qy        865 CTCAGACCCTGGGGGCCCAGTCAATGGGTACCAGAAAATAACAGGGGGCCCTGGGCTTAT 924
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        995 CTCAGACCCTGGGGGCCCAGTCAATGGGTACCAGAAAATAACAGGGGGCCCTGGGCTTAT 1054

Qy        925 CAACGGACGCCATGCTAAAATTGGCACCGTGGTGTCTTTCTTTTGTAACAACTCCTATGT 984
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1055 CAACGGACGCCATGCTAAAATTGGCACCGTGGTGTCTTTCTTTTGTAACAACTCCTATGT 1114

Qy        985 TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGGAAACAGCC 1044
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1115 TCTTAGTGGCAATGAGAAAAGAACTTGCCAGCAGAATGGAGAGTGGTCAGGGAAACAGCC 1174

Qy       1045 CATCTGCATAAAAGCCTGCCGAGAACCAAAGATTTCAGACCTGGTGAGAAGGAGAGTTCT 1104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1175 CATCTGCATAAAAGCCTGCCGAGAACCAAAGATTTCAGACCTGGTGAGAAGGAGAGTTCT 1234

Qy       1105 TCCGATGCAGGTTCAGTCAAGGGAGACACC 1134
              |||||||||||||||||||||||||||||
Db       1235 TCCGATGCAGGTTCAGTCAAGGGAGACACC 1264


RESULT 6
US-09-537-654-3
; Sequence 3, Application US/09537654
; Patent No. 6720478
; GENERAL INFORMATION:
;  APPLICANT: Mahajan, Pramod B.
;  APPLICANT: Shi, Jinrui
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Db       1191 GCCAGTCGGGATCTCAGCACTTCCTTCCAGGAGTCCCACATCACTGTGGCTGGCTGGAAT 1250

Qy        603 ValLeuAlaAspValArgSerProGlyPheLysAsnAspThrLeuArgSerGlyValVal 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 GTCCTGGCAGACGTGAGGAGCCCTGGCTTCAAGAACGACACACTGCGCTCTGGGGTGGTC 1310

Qy        623 SerValValAspSerLeuLeuCysGluGluGlnHisGluAspHisGlyIleProValSer 642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 AGTGTGGTGGACTCGCTGCTGTGTGAGGAGCAGCATGAGGACCATGGCATCCCAGTGAGT 1370

Qy        643 ValThrAspAsnMetPheCysAlaSerTrpGluProThrAlaProSerAspIleCysThr 662
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 GTCACTGATAACATGTTCTGTGCCAGCTGGGAACCCACTGCCCCTTCTGATATCTGCACT 1430

Qy        663 AlaGluThrGlyGlyIleAlaAlaValSerPheProGlyArgAlaSerProGluProArg 682
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1431 GCAGAGACAGGAGGCATCGCGGCTGTGTCCTTCCCGGGACGAGCATCTCCTGAGCCACGC 1490

Qy        683 TrpHisLeuMetGlyLeuValSerTrpSerTyrAspLysThrCysSerHisArgLeuSer 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1491 TGGCATCTGATGGGACTGGTCAGCTGGAGCTATGATAAAACATGCAGCCACAGGCTCTCC 1550

Qy        703 ThrAlaPheThrLysValLeuProPheLysAspTrpIleGluArgAsnMetLys 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1551 ACTGCCTTCACCAAGGTGCTGCCTTTTAAAGACTGGATTGAAAGAAATATGAAA 1604

RESULT 5
US-09-280-116-179
; Sequence 179, Application US/09280116A
; Patent No. 6331427
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  TITLE OF INVENTION: Nucleic Acid Molecules Encoding Human Protease Homologs
;  FILE REFERENCE: 5800-24, 035800/176965
;  CURRENT APPLICATION NUMBER: US/09/280,116A
;  CURRENT FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 268
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 179
;  LENGTH: 505
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  OTHER INFORMATION: asticin/m 12a metalloproteases
US-09-280-116-179

Alignment Scores:
Pred. No.:              5.5e-81       Length:          505
Score:                  893.00        Matches:         166
Percent Similarity:     98.81%        Conservative:    0
Best Local Similarity:  98.81%        Mismatches:      1
Query Match:            22.64%        Indels:          2
DB:                     3             Gaps:            0

US-10-063-692-38 (1-720) x US-09-280-116-179 (1-505)

Qy        103 LeuAspAspPheTyrValLysGlyPheTyrCysAlaGluCysArgAlaGlyTrpTyrGly 122
              ||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||||
Db          3 TTGGATGACTTCTATGTGAAGGGGTTCTACTGTGCAGAGTGCCGAGCAGC-TGGTACGGA 61

Qy        123 GlyAspCysMetArgCysGlyGlnValLeuArgAlaProLysGlyGlnIleLeuLeuGlu 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 GGAGACTGCATGCGATGTGGCCAGGTTCTGCGAGCCCCAAAGGGTCAGATTTTGTTGGAA 121

Qy        143 SerTyrProLeuAsnAlaHisCysGluTrpThrIleHisAlaLysProGlyPheValIle 162
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AGCTATCCCCTAAATGCTCACTGTGAATGGACCATTCATGCTAAACCTGGGTTTGTCATC 181

Qy        163 GlnLeuArgPheValMetLeuSerLeuGluPheAspTyrMetCysGlnTyrAspTyrVal 182
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAACTAAGATTTGTCATGTTGAGCCTGGAGTTTGACTACATGTGCCAGTATGACTATGTT 241

          183 GluValArgAspGlyAspAsnArgAspGlyGlnIleIleLysArgValCysGlyAsnGlu 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 GAGGTTCGTGATGGAGACAACCGCGATGGCCAGATCATCAAGCGTGTCTGTGGCAACGAG 301

Qy        203 ArgProAlaProIleGlnSerIleGlySerSerLeuHisValLeuPheHisSerAspGly 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 CGGCCAGCTCCTATCCAGAGCATAGGATCCTCACTCCACGTCCTCTTCCACTCCGATGGC 361

Qy        223 SerLysAsnPheAspGlyPheHisAlaIleTyrGluGluIleThrAlaCysSerSerSer 242
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 TCCAAGAATTTTGACGGTTTCCATGCCATTTATGAGGAGATCACAGCATGCTCCTCATCC 421

Qy        243 ProCysPheHisAspGlyThrCysValLeuAspLysAlaGlySerTyr-LysCysAlaCy 262
              ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db        422 CCTTGTTTCCATGACGGCACGTGCGTCCTTGACAAGGCTGGATCTTACAAAGTGTGCCTG 481

Qy        262 sLeuAlaGlyTyrThrGlyGln 269
              |||||||||||||||||||||||
Db        482 CTTGGCAGGCTATACTGGGCAG 503

RESULT 6
US-08-296-014A-3
; Sequence 3, Application US/08296014A
; Patent No. 5716834
;  GENERAL INFORMATION:
;    APPLICANT:  Ding, Jeak Ling
;    APPLICANT:  Ho, Bow
;    TITLE OF INVENTION:  The Cloned Factor C cDNA of the
;    TITLE OF INVENTION:  Singapore Horseshoe Crab, Carcinoscorpius
;    TITLE OF INVENTION:  rotundicauda and Purification of Factor C Proenzyme
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Birch, Stewart, Kolasch & Birch
;      STREET:  8110 Gatehouse Road, Suite 500 East
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22042
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/296,014A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murphy, Jr., Gerald M.
;      REGISTRATION NUMBER:  28,977
;      REFERENCE/DOCKET NUMBER:  1781-105P
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3448 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  both
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Carcinoscorpius rotundicauda
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  18..3074
US-08-296-014A-3

Alignment Scores:
Pred. No.:              1.58e-56      Length:          3448
Score:                  665.00        Matches:         222
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